BIOTECHNOLOGY SYSTEMS BRANCH

# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/889,344ASource: 01PEDate Processed by STIC: 7-22-02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:
  U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
  Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
  - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1803, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/889344	
ATTN: NEW RULES CASES	:: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SO	OFTWARE
lWrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6PatentIn 2.0 "bug"	A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)  Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	••• ·
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8Skipped Sequences' (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
0Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
1Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	·
2PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
3Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

## Raw Sequence Listing Error Summary.

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: $09/889,344$
ATTN: NEW RULES CASES	: Please disregard english "Alpha" headers, Which were inserted by PTO software
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2hvalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
(NEW RULES).	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
(NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
"bug"	Please do not use "Copy to Disk" function f Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated n raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
	AMC - Biotechnology Systems Branch - 06/04/2001

### Does Not Comply Corrected Diskette Needed



OIPE

**RAW SEQUENCE LISTING**PATENT APPLICATION: **US/09/889,344A**DATE: 07/22/2002

TIME: 10:40:33

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\I889344A.raw

```
4 <110> APPLICANT: CHEN, WENFANG
      5
              MEEK, THOMAS D.
              POWELL, DAVID J.
      6
      7
              TEW, DAVID G.
     10 <120> TITLE OF INVENTION: Method of Site Specific Labeling of Proteins and Uses
              Therefor
     11
     14 <130> FILE REFERENCE: P50892
     16 <140> CURRENT APPLICATION NUMBER: 09/889,344A
     17 <141> CURRENT FILING DATE: 2001-07-16
     19 <150> PRIOR APPLICATION NUMBER: PCT/US00/01481
     20 <151> PRIOR FILING DATE: 2000-01-20
     22 <150> PRIOR APPLICATION NUMBER: US 60/117,327
     23 <151> PRIOR FILING DATE: 1999-01-22
     25 <160> NUMBER OF SEQ ID NOS: 16
     27 <170> SOFTWARE: FastSEQ for Windows Version 3.0
     29 <210> SEQ ID NO: 1
     30 <211> LENGTH: 5
     31 <212> TYPE: PRT
     32 <213> ORGANISM: Artificial Sequence
     34 <220> FEATURE:
     35 <221> NAME/KEY: unsure
     36 <222> LOCATION: (5)
     37 <223> OTHER INFORMATION: Where Xaa at\position (5) can represent Leucine or Isoleucine
     39 <400> SEQUENCE: 1
W--> 40 Gln Ser Lys Val Xaa
     41
     43 <210> SEQ ID NO: 2
                                                 See Hen # 11 on ERROR
Summary SHEET
     44 <211> LENGTH: 207
     45 <212> TYPE: PRT
     46 <213> ORGANISM: Artificial Sequence
     48 <220> FEATURE:
     49 <221> NAME/KEY: unsure
     50 <222> LOCATION: (1)(2)(3)(4)(5)(6)(7)(8)(9)(10)(11)(12)(13)(14)(15)
     51 <222> LOCATION: (16)(17)(18)(19)(20)(21)(22)(23)(24)(25)(26)(27)(28)
W--> 52 <222> (29)(30)(31)(32)(33)(34)(35)(36)(37)(38)(39)(40)(41)
W--> 53 <222> (42)(43)(44)(45)(46)(47)(48)(49)(50)(51)(52)(53)(54)
W--> 54 < 222 > (55)(56)(57)(58)(59)(60)(61)(62)(62)(64)(65)(66)(67)
W-->55 < 222 > (68)(69)(70)(71)(72)(73)(74)(75)(76)(77)(78)(79)(80)
W--> 56 < 222 > (81)(82)(83)(84)(85)(86)(87)(88)(89)(90)(91)(92)(93)
W--> 57 < 222 > (94)(95)(96)(97)(98)(99)(100)(101)(106)(107)(108)(109)
W--> 58 < 222 > (110)(111)(112)(113)(114)(115)(116)(117)(118)(119)(120)
W--> 59 < 222 > (121)(122)(123)(124)(125)(126)(127)(128)(129)(130)(131)
W--> 60 <222> (132)(133)(134)(135)(136)(137)(138)(139)(140)(141)(142)
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RAW SEQUENCE LISTING DATE: 07/22/2002 PATENT APPLICATION: US/09/889,344A TIME: 10:40:33

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\1889344A.raw

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W--> 62 < 222 > (154)(155)(156)(157)(158)(159)(160)(161)(162)(163)(164)
W--> 63 < 222 > (165)(166)(167)(168)(169)(170)(171)(172)(173)(174)(175)
W--> 64 < 222 > (176)(177)(178)(179)(180)(181)(182)(183)(184)(185)(186)
W--> 65 < 222 > (187)(188)(189)(190)(191)(192)(193)(194)(195)(196)(197)
W--> 66 < 222 > (198)(199)(200)(201)(202)(203)(204)(205)(206)(207)
   67 <223> OTHER INFORMATION: Where Xaa can represent none or any one of the twenty
naturally
   68 <223> OTHER INFORMATION: occurring amino acids
W--> 70 <400> 2
W--> 71
      72
W--> 73
      74
                            25
W--> 75
      76
W--> 77
      78
W--> 79
      80
W--> 81
      82
                 85
                               90
W--> 83
      Xaa Xaa Xaa Xaa Gln Ser Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
   84
                            105
                                          110
W--> 85
      86
                         120
W--> 87
      88
         130
                      135
                                     140
W--> 89
      90
                    150
                                  155
W--> 91
      92
                 165
                               170
W--> 93
      94
W--> 95
      96
           195
   98 <210> SEQ ID NO: 3
   99 <211> LENGTH: 207
                                   See , ten # 11
   100 <212> TYPE: PRT;
                                    ERROR SUMMARY SHEET
   101 <213> ORGANISM: Artificial Sequence
   103 <220> FEATURE:
   104 <221> NAME/KEY: unsure
   105 < 222 > LOCATION: (1)(2)(3)(4)(5)(6)(7)(8)(9)(10)(11)(12)(13)(14)(15)
   106 < 222 > LOCATION: (16)(17)(18)(19)(20)(21)(22)(23)(24)(25)(26)(27)(28)
W--> 107 < 222> (29)(30)(31)(32)(33)(34)(35)(36)(37)(38)(39)(40)(41)
W--> 108 < 222 > (42)(43)(44)(45)(46)(47)(48)(49)(50)(51)(52)(53)(54)
W--> 109 <222> (55)(56)(57)(58)(59)(60)(61)(62)(62)(64)(65)(66)(67)
W--> 110 \langle 222 \rangle (68)(69)(70)(71)(72)(73)(74)(75)(76)(77)(78)(79)(80)
W--> 111 < 222> (81)(82)(83)(84)(85)(86)(87)(88)(89)(90)(91)(92)(93)
W--> 112 < 222> (94)(95)(96)(97)(98)(99)(100)(101)(106)(107)(108)(109)
```

DATE: 07/22/2002

TIME: 10:40:33

Input Set : A:\USSEQLIST2.txt Output Set: N:\CRF3\07222002\1889344A.raw  $W--> 113 \langle 222 \rangle (110)(111)(112)(113)(114)(115)(116)(117)(118)(119)(120)$  $W--> 114 \langle 222 \rangle (121)(122)(123)(124)(125)(126)(127)(128)(129)(130)(131)$ W--> 115 < 222 > (132)(133)(134)(135)(136)(137)(138)(139)(140)(141)(142)W--> 116 < 222 > (143)(144)(145)(146)(147)(148)(149)(150)(151)(152)(153) $W--> 117 \langle 222 \rangle (154)(155)(156)(157)(158)(159)(160)(161)(162)(163)(164)$ W--> 118 < 222> (165)(166)(167)(168)(169)(170)(171)(172)(173)(174)(175)W--> 119 < 222> (176)(177)(178)(179)(180)(181)(182)(183)(184)(185)(186)W--> 120 < 222> (187)(188)(189)(190)(191)(192)(193)(194)(195)(196)(197) $W--> 121 \langle 222 \rangle (198)(199)(200)(201)(202)(203)(204)(205)(206)(207)$ 122 <223> OTHER INFORMATION: Where Xaa can represent none or any one of the twenty naturally 123 <223> OTHER INFORMATION: occurring amino acids W--> 125 < 400> 3127 W--> 128 129 25 20 W--> 130 131 W--> 132133 50 W--> 134135 W--> 136 137 90 W--> 138 Xaa Xaa Xaa Xaa Gln Ser Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa 139 105 100 W--> 140125 141 120 W--> 142143 135 140 130 W--> 144 145 150 W--> 146 147 165 170 W--> 148149 185 W--> 150 151 195 200 205 153 <210> SEQ ID NO: 4 154 <211> LENGTH: 10 155 <212> TYPE: PRT 156 <213> ORGANISM: Artificial Sequence 158 <220> FEATURE: 159 <223> OTHER INFORMATION: Derivative of a factor XIII substrate 161 <400> SEQUENCE: 4 162 Leu Ser Leu Ser Gln Ser Lys Val Leu Gly 165 <210> SEQ ID NO: 5 166 <211> LENGTH: 10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/889,344A

RAW SEQUENCE LISTING DATE: 07/22/2002 PATENT APPLICATION: US/09/889,344A TIME: 10:40:33

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\1889344A.raw

167 <212> TYPE: PRT 168 <213> ORGANISM: Artificial Sequence 170 <220> FEATURE: 171 <223> OTHER INFORMATION: Derivative of a factor XIII substrate 173 <400> SEQUENCE: 5 174 Ile Gly Glu Gly Gln Ser Lys Val Leu Gly 175 177 <210> SEQ ID NO: 6 178 <211> LENGTH: 10 179 <212> TYPE: PRT 180 <213> ORGANISM: Artificial Sequence 182 <220> FEATURE: 183 <223> OTHER INFORMATION: Derivative of a factor XIII substrate 185 <400> SEQUENCE: 6 186 Leu Gly Pro Gly Gln Ser Lys Val Ile Gly 5 189 <210> SEQ ID NO: 7 190 <211> LENGTH: 81 191 <212> TYPE: DNA 192 <213> ORGANISM: Unknown 194 <220> FEATURE: 195 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag 197 <400> SEQUENCE: 7 198 tgtacctcag accatatgag cctgtccctg tcccagtcca aagttctgcc gggtccgagc 60 199 actatcgaag aacgcgttaa g 81 201 <210> SEQ ID NO: 8 202 <211> LENGTH: 37 203 <212> TYPE: DNA 204 <213> ORGANISM: Unknown 206 <220> FEATURE: 207 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag 209 <400> SEQUENCE: 8 37 210 tgatgtcagt caagcttacg cctggtggcc gttgatg 212 <210> SEQ ID NO: 9 213 <211> LENGTH: 14 214 <212> TYPE: PRT 215 <213> ORGANISM: Artificial Sequence 217 <220> FEATURE: 218 <223> OTHER INFORMATION: Derivative of a factor XIII substrate 220 <400> SEQUENCE: 9 221 Met Ser Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro 224 <210> SEQ ID NO: 10 225 <211> LENGTH: 37 226 <212> TYPE: DNA 227 <213> ORGANISM: Unknown 229 <220> FEATURE:

230 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag

232 <400> SEQUENCE: 10

RAW SEQUENCE LISTING DATE: 07/22/2002 PATENT APPLICATION: US/09/889,344A TIME: 10:40:33

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\1889344A.raw

233 tgtacctcag accatatgag cactatcgaa gaacgcg 37 235 <210> SEQ ID NO: 11 236 <211> LENGTH: 78 237 <212> TYPE: DNA 238 <213> ORGANISM: Unknown 240 <220> FEATURE: 241 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag 243 <400> SEQUENCE: 11 244 tgatgtcagt caagettacg gacceggeag aactttggae tgggacaggg acagegeetg 60 245 gtggccgttg atgtaatc 78 247 <210> SEQ ID NO: 12 248 <211> LENGTH: 12 249 <212> TYPE: PRT 250 <213> ORGANISM: Artificial Sequence 252 <220> FEATURE: 253 <223> OTHER INFORMATION: Derivative of E. coli ACP protein 255 <400> SEQUENCE: 12 256 Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro 257 1 5 259 <210> SEO ID NO: 13 260 <211> LENGTH: 92 261 <212> TYPE: DNA 262 <213> ORGANISM: Unknown 264 <220> FEATURE: 265 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag into Streptococcus haemophilus FabH gene 268 <400> SEQUENCE: 13 269 tatcatatga geetgteeet gteecagtee aaagttetge egggteeggg taccetegag 60 270 ggatccgctt ttgcaaaaat aagtcaggtt gc 92 272 <210> SEQ ID NO: 14 273 <211> LENGTH: 53 274 <212> TYPE: DNA 275 <213> ORGANISM: Unknown 277 <220> FEATURE: 278 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag into 279 Streptococcus haemophilus FabH gene 281 <400> SEQUENCE: 14 282 ctcagatctg agctcactag tggatcctta aattgtaaga atgagcgtgc ccc 53 284 <210> SEQ ID NO: 15 285 <211> LENGTH: 364 286 <212> TYPE: PRT 287 <213> ORGANISM: Artificial Sequence 289 <220> FEATURE: 290 <223> OTHER INFORMATION: Modified sequence of Streptococus haemophilus FabH 292 <400> SEQUENCE: 15 293 Met Gly His His His His His His His His His Ser Ser Gly His 294 1 5 10 15 295 Ile Glu Gly Arg His Met Ser Leu Ser Leu Ser Gln Ser Lys Val Leu 296

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/22/2002 PATENT APPLICATION: US/09/889,344A TIME: 10:40:34

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\1889344A.raw

#### Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:1; Xaa Pos. 5
Seq#:2; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:2; Xaa Pos. 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41
Seq#:2; Xaa Pos. 42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60
Seq#:2; Xaa Pos. 61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79
Seq#:2; Xaa Pos. 80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98
Seq#:2; Xaa Pos. 99,100,101,106,107,108,109,110,111,112,113,114,115,116,117
Seq#:2; Xaa Pos. 118,119,120,121,122,123,124,125,126,127,128,129,130,131
Seq#:2; Xaa Pos. 132,133,134,135,136,137,138,139,140,141,142,143,144,145
Seq#:2; Xaa Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159
Seq#:2; Xaa Pos. 160,161,162,163,164,165,166,167,168,169,170,171,172,173
Seq#:2; Xaa Pos. 174,175,176,177,178,179,180,181,182,183,184,185,186,187
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Seg#:2; Xaa Pos. 202,203,204,205,206,207
Seq#:3; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:3; Xaa Pos. 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41
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Seq#:3; Xaa Pos. 80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98
Seq#:3; Xaa Pos. 99,100,101,106,107,108,109,110,111,112,113,114,115,116,117
\overline{\texttt{Seq\#:3;}} \hspace*{0.2cm} \textbf{Xaa Pos.} \hspace*{0.2cm} 118,119,120,121,122,123,124,125,126,127,128,129,130,131}
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Seq#:3; Xaa Pos. 160,161,162,163,164,165,166,167,168,169,170,171,172,173
Seq#:3; Xaa Pos. 174,175,176,177,178,179,180,181,182,183,184,185,186,187
Seq#:3; Xaa Pos. 188,189,190,191,192,193,194,195,196,197,198,199,200,201
Seq#:3; Xaa Pos. 202,203,204,205,206,207
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### VERIFICATION SUMMARY PATENT APPLICATION: US/09/889,344A DATE: 07/22/2002 TIME: 10:40:34

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\1889344A.raw

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L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:52 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:53 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:55 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:60 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:61 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:62 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:63 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:64 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:66 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:70 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:16
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:32 L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:48
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:64
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:80
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:96
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:112
L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:128 L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:144 L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:160
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:176
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:192
L:107 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:108 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:109 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:110 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3 L:111 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:112 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:113 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:114 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:115 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:117 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3 L:118 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:119 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:120 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:121~M:258~W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:125 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
```

#### VERIFICATION SUMMARY

PATENT APPLICATION: US/09/889,344A

DATE: 07/22/2002 TIME: 10:40:34

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\1889344A.raw

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L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:32
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:48
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:64
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:80
L:138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:96
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:112
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:128
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:144
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:160
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:176
L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:176
```